

DATE: Tuesday, May 07, 2002

Set Nam	<u>ne</u> <u>Query</u> le	Hit Count	Set Name result set
DB=U	JSPT,PGPB; PLUR=YES; OP=ADJ		
1.4	L3 or l2	54	L4
L3	(ashkenazi-a\$.in. or chunthar\$.in. or kim-\$k.in.) and (trail or apo\$2)	7	L3
L2	L1 and (trail or apo-2 or apo2)	52	L2
L1	tr6 or trick2 or trick-2 or apo2 or apo-2 or tango63e or (tango adj 63e) or dr5 or trail2 or trail-2	1464	L1

END OF SEARCH HISTORY

```
W95538; Comparison of death domains (76 aa long)
   AC
   DT
        25-MAR-1999 (first entry)
        Death domain containing receptor polypeptide (DR3).
   DΕ
        Death domain; receptor; DR3-V1; DR3; recombinant.
   KW
   OS
        Homo sapiens.
   FH
        Key
                       Location/Qualifiers
  FT
        Peptide
                        1..24
  FT
                        /note= "signal peptide"
  FT
       Protein
                       25..417
  FT
                       /note= "mature protein"
  PN
       J11000170-A.
  PD
       06-JAN-1999.
  PF
       12-MAR-1997; 057503.
  PR
       06-FEB-1997; US-037341.
  PR
       12-MAR-1996; US-013285.
  PR
       17-OCT-1996; US-028711.
       (HUMA-) HUMAN GENOME SCI INC.
  PΑ
       (UNMI ) UNIV MICHIGAN.
  PΑ
       WPI; 99-124390/11.
  DR
  DR
       N-PSDB; X00925.
       New death domain containing receptor and recombinant vector -
  PΤ
       optionally comprising leader sequence
  PT
       Claim 1; Fig 3; 50pp; Japanese.
  PS
      The invention provides nucleotide sequences encoding death domain
  CC
      containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
 CC
      is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
 CC
      contained in ATCC deposition No. 97757. Recombinant vectors comprising
 CC
      the nucleic acid sequences and optionally the leader sequences are used
 CC
      for the recombinant production of the proteins. The present sequence
 CC
      represents the amino acid sequence of a death domain containing receptor
 CC
 CC
      polypeptide (DR3).
 SQ
      Sequence
                 417 AA;
   Query Match
                          24.3%; Score 133; DB 39; Length 417;
   Best Local Similarity 34.4%; Pred. No. 9.10e-03;
              22; Conservative
                                  12; Mismatches 28; Indels 2; Gaps
                                                                            1;
 Db
       340 davparrwkefvrtlglreaeieaveveigrfrdqqyemlkrw--rqqqpaglgavyaal 397
           1 11 1 ::1 111 : 11
                                     1: 11 11:1: : : 1:::: 11
        3 DLVPFDSWEPLMRKLGLMDNEIKVAKAEAAGHRDTLYTMLIKWVNKTGRDASVHTLLDAL 62
· Qy
 Db
       398 ermg 401
           1:1
Qу
       63 ETLG 66
```